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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/810,521

DATE: 08/28/2001

TIME: 11:50:38

Input Set : A:\Ma278416.app

Output Set: N:\CRF3\08282001\I810521.raw

3 <110> APPLICANT: KREUTZER, CAROLINE
 4 MOCKEL, BETTINA
 5 PFEFFERLE, WALTER
 6 EGGELING, LOTHAR
 7 SAHM, HERMANN
 8 PATEK, MIROSLAV
 10 <120> TITLE OF INVENTION: L-LYSINE PRODUCING CORYNEBACTERIA AND
 11 PROCESS FOR THE PREPARATION OF LYSINE
 13 <130> FILE REFERENCE: 21123/278416/MAS
 15 <140> CURRENT APPLICATION NUMBER: 09/810,521
 16 <141> CURRENT FILING DATE: 2001-03-19
 18 <150> PRIOR APPLICATION NUMBER: DE 199 31314.8
 19 <151> PRIOR FILING DATE: 1999-05-07
 21 <160> NUMBER OF SEQ ID NOS: 18
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 795
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Corynebacterium glutamicum
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 31 <221> NAME/KEY: -35_signal
 32 <222> LOCATION: (774)..(779)
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: DNA upstream from dapB
 37 <400> SEQUENCE: 1
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 39 acggggttca aaaatactgg tgaagttgat gtcttcaaca atgcctgcac caggatatga 120
 40 tccgggtatcg atacctggaa cgacaacctg atcaggatat ccagtgcctt gaattattgac 180
 41 gttgaggaag gaatcaccag ccatctcaac tggaagacct gacgcctgct gaattggatc 240
 42 agtggcccaa tcgaccacc aaccagggtg gccattaccg gcgatatcaa aaacaactcg 300
 43 tgtgaacggt tcgtgctcgg caacgcggat gccagcgatc gacatatcgg agtcaccaac 360
 44 ttgagcctgc tgcttctgat ccatcgacgg ggaacccaac ggcggcaaag cagtggggga 420
 45 aggggggagt ttggtgcact ctgaaccgag tgggtctctga agtggtaggc gacggggcag 480
 46 ctatctgaag gcgtgcgagt tgtggtgacc gggttagcgg tttcagtttc tgtcacaact 540
 47 ggagcaggac tagcagaggt tgtaggcgtt gagccgcttc catcacaagc acttaaaagt 600
 48 aaagaggcgg aaaccacaag cgccaaggaa ctactgcgga acggggcgtg aaggggcaact 660
 49 taagtctcat atttcaaaca tagttccacc tgtgtgatta atccctagaa cggaacaaac 720
 50 tgatgaacaa tcgttaacaa cacagaccaa aacggtcagt taggtatgga tatcagcacc 780
 51 ttctgaacgg gtacg
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 1815
 56 <212> TYPE: DNA
 57 <213> ORGANISM: Corynebacterium glutamicum
 59 <220> FEATURE:
 60 <221> NAME/KEY: -35_signal
 61 <222> LOCATION: (774)..(779)
 63 <220> FEATURE:

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64 <221> NAME/KEY: -10_signal
65 <222> LOCATION: (798)..(803)
67 <220> FEATURE:
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69 <222> LOCATION: (851)..(1594)
71 <400> SEQUENCE: 2
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74 acgggcttca aaaatactgg tgaagttgat gtcttcaaca atgcctgcac caggatatga 120
76 tccggtatcg atacctggaa cgacaacctg atcaggatat ccagtgcctt gaattattgac 180
78 gttgaggaag gaatcaccag ccattctcaac tggagacact gacgcctgct gaattggatc 240
80 agtggcccaa tcgacccacc aaccagggtg gccattaccg gcgatatcaa aaacaactcg 300
82 tgtgaacgtt tcgtgctcgg caacgcggat gccagcgatc gacatatcgg agtcaccaac 360
84 ttgagcctgc tgcttctgat ccacgcacgg ggaacccaac ggcggaagag cagtggggga 420
86 aggggggagt ttggtgcact ctgaaccgag tgggtctctga agtggtaggc gacggggcag 480
88 ctatctgaag gcgtgcgagt tgtggtgacc ggggttagcgg ttccagtttc tgtcacaact 540
90 ggagcaggac tagcagaggt ttaggcgtt gagccgcttc catcacaagc acttaaaagt 600
92 aaagaggcgg aaaccacaag cgccaaggaa ctactgcgga acgggcggtg aagggaact 660
94 taagtctcat atttcaaaca tagttccacc tgtgtgatta atccctagaa cggaacaaac 720
96 tgatgaacaa tcgttaacaa cacagaccaa aacgggtcagt taggtatgga tatcagcacc 780
98 ttctgaacgg gtacgtctag actggtgggc gtttgaaaaa ctcttcgccc cacgaaaatg 840
100 aaggagcata atg gga atc aag gtt ggc gtt ctc gga gcc aaa ggc cgt 889
101 Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg
102 1 5 10
104 gtt ggt caa act att gtg gca gca gtc aat gag tcc gac gat ctg gag 937
105 Val Gly Gln Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu
106 15 20 25
108 ctt gtt gca gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac 985
109 Leu Val Ala Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp
110 30 35 40 45
112 aac ggc gct gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg 1033
113 Asn Gly Ala Glu Val Val Val Asp Phe Thr Pro Asn Ala Val Met
114 50 55 60
116 ggc aac ctg gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga 1081
117 Gly Asn Leu Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly
118 65 70 75
120 acc acg ggc ttc gat gat gct cgt ttg gag cag gtt cgc gac tgg ctt 1129
121 Thr Thr Gly Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu
122 80 85 90
124 gaa gga aaa gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc 1177
125 Glu Gly Lys Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile
126 95 100 105
128 tct gcg gtg ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc 1225
129 Ser Ala Val Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe
130 110 115 120 125
132 gaa tca gct gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca 1273
133 Glu Ser Ala Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala
134 130 135 140
136 cct tca ggc acc gcg atc cac act gct cag ggc att gct gcg gca cgc 1321
137 Pro Ser Gly Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg

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138          145          150          155
140 aaa gaa gca ggc atg gac gca cag cca gat gcg acc gag cag gca ctt 1369
141 Lys Glu Ala Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu
142          160          165          170
144 gag ggt tcc cgt ggc gca agc gta gat gga atc ccg gtt cat gca gtc 1417
145 Glu Gly Ser Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val
146          175          180          185
148 cgc atg tcc ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag 1465
149 Arg Met Ser Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln
150 190          195          200          205
152 ggt cag acc ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt 1513
153 Gly Gln Thr Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe
154          210          215          220
156 gca cca ggt gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc 1561
157 Ala Pro Gly Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly
158          225          230          235
160 cta gtc gta gga ctt gag cat tac cta ggc ctg taaaggctca tttcagcagc 1614
161 Leu Val Val Gly Leu Glu His Tyr Leu Gly Leu
162          240          245
164 ggggtggaatt ttttaaaagg agcgttttaa ggctgtggcc gaacaagtta aattgagcgt 1674
166 ggagttgata gcgtgcagtt cttttactcc acccgctgat gttgagtggc caactgatgt 1734
168 tgagggcgcg gaagcactcg tcgagtttgc gggtcgtgcc tgctacgaaa cttttgataa 1794
170 gccgaaccct cgaactgctt c 1815
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 248
175 <212> TYPE: PRT
176 <213> ORGANISM: Corynebacterium glutamicum
178 <400> SEQUENCE: 3
179 Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
180 1 5 10 15
182 Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
183 20 25 30
185 Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
186 35 40 45
188 Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
189 50 55 60
191 Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
192 65 70 75 80
194 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
195 85 90 95
197 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
198 100 105 110
200 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
201 115 120 125
203 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
204 130 135 140
206 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
207 145 150 155 160
209 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser

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210                               165                               170                               175
212 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
213                               180                               185                               190
215 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
216                               195                               200                               205
218 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
219                               210                               215                               220
221 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
222 225                               230                               235                               240
224 Gly Leu Glu His Tyr Leu Gly Leu
225                               245
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229 <211> LENGTH: 79
230 <212> TYPE: DNA
231 <213> ORGANISM: Corynebacterium glutamicum
233 <220> FEATURE:
234 <223> OTHER INFORMATION: dapA wild-type promoter
236 <400> SEQUENCE: 4
237 gtttaggtttt ttgcgggggtt gtttaacccc caaatgaggg aagaaggtaa ccttgaactc 60
238 tatgagcaca ggtttaaca
241 <210> SEQ ID NO: 5
242 <211> LENGTH: 79
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Description of Artificial Sequence:
248     dapA promoter of C. glutamicum with the ✓
249     MC20 mutation
251 <220> FEATURE:
252 <221> NAME/KEY: mutation
253 <222> LOCATION: (45)
255 <400> SEQUENCE: 5
256 gtttaggtttt ttgcgggggtt gtttaacccc caaatgaggg aagatggtaa ccttgaactc 60
257 tatgagcaca ggtttaaca
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 80
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence:
267     dapA promoter of C. glutamicum with the ✓
268     MA16 mutation
271 <220> FEATURE:
272 <221> NAME/KEY: mutation
273 <222> LOCATION: (35)..(53)
275 <400> SEQUENCE: 6
276 gttagggtttt ttgcgggggtt gtttaacccc caaatgagg gaagaaggta taattgaact 60
277 ctatgagcac aggtttaaca
280 <210> SEQ ID NO: 7

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281 <211> LENGTH: 28
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283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
287     Primer
289 <400> SEQUENCE: 7
290 ctcgagagcg gatccgcgct gactcacc                28
293 <210> SEQ ID NO: 8
294 <211> LENGTH: 27
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
300     Primer
302 <400> SEQUENCE: 8
303 ggagagtacg gcggatccac cgtgacc                27
306 <210> SEQ ID NO: 9
307 <211> LENGTH: 19
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
313     Primer
315 <400> SEQUENCE: 9
316 gaacgccaac cttgattcc                19
319 <210> SEQ ID NO: 10
320 <211> LENGTH: 19
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
326     Primer
328 <400> SEQUENCE: 10
329 ctttgccgcc gttgggttc                19
332 <210> SEQ ID NO: 11
333 <211> LENGTH: 24
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
339     Primer
341 <400> SEQUENCE: 11
342 aagcttaggt tgtaggcgtt gagg                24
345 <210> SEQ ID NO: 12
346 <211> LENGTH: 20
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:

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VERIFICATION SUMMARY

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